

Claims

1. A method for transforming a plant cell which comprises:
 - (a) selecting at least one cell from a Type I, Type
5 II, hypocotyl-derived, or cotyledon-derived callus culture or from a meristem, pollen, cotyledon, or germ cell tissue; and
 - (b) inserting DNA into said cell by whisker mediated transformation.
- 10 2. A method for producing a fertile transgenic plant which comprises regenerating a cell produced by the method of claim 1.
3. A method for producing a fertile transgenic plant comprising the steps of: (i) establishing a regenerable
15 callus culture from a plant to be transformed wherein said callus culture is selected from the group consisting of Type I, Type II, hypocotyl-derived, and cotyledon-derived callus culture; (ii) selecting a plant cell aggregate therefrom for transformation; (iii) transforming said
20 plant cell aggregate with DNA by whisker-mediated transformation; (iv) identifying transformed cell lines therefrom; and (iv) regenerating fertile transgenic plants therefrom.
4. The method of Claim 3 wherein said Type I callus
25 culture is established from *Zea mays* or *Oryza sativa*.
5. The method of Claim 3 wherein said Type II callus culture is established from *Zea mays*.
6. The method of Claim 3 wherein said hypocotyl-derived culture is established from *Gossypium hirsutum*.
- 30 7. The method of Claim 3 wherein said cotyledon-derived culture is established from *Gossypium hirsutum*.
8. The method of Claim 3 wherein said plant cell aggregate is initiated on solid medium.
9. A fertile transgenic plant produced by the method of
35 of claim 3.

10. A DNA construct functional in a plant cell comprising
in the 5' to 3' direction of transcription, a
transcriptional regulatory region functional in said plant
cell and having a DNA sequence according to SEQ ID NO:1,
5 and a gene of interest, said gene being either in the
sense or antisense orientation.

11. The transcriptional regulatory region according to
Claim 10 comprising the DNA sequence SEQ ID NO:1.